

AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph on page 27, line 32 to page 28, line 2, as follows:

The term "neighboring" means in the context of the present invention the shortest distance between two positions in a crystal structure being prepared, e.g., as described in "Protein Crystallization Techniques, Strategies, and Tips", A Laboratory Manual by Terese M. Bergfors), or as describe on the Internet on the site: ~~www.hamptonresearch.com~~ hamptonresearch.com.

Please amend the paragraph on page 32, lines 3-15, as follows:

Protein structure databases, such as "The Protein Data Bank (PDB) (~~http://www.pdb.bnl.gov/~~) pdb.bnl.gov/" or "The Brookhaven databank at Brookhaven National Laboratory, US" are search for proteins similar to the molecule in question that a model are to be build of. The amino acid sequences are aligned taking structurally conserved regions into consideration and the coordinates are copied from the reference protein to the subject protein. The coordinates for regions with insertions and deletions are assigned either from other proteins having similar amino acid sequence, or by using the random structure generator function found in most 3D software packages, eg. in Homology from Blosym, MSI.